

1

SEQUENCE LISTING

<110> Regents of the University of Minnesota et al.

5

<120> Streptococcal C5a peptidase vaccine

<130> 600.450WO1

10 <150> US 09/206,898

<151> 1998-12-07

<150> US 08/589,756

<151> 1996-01-22

15

<160> 23

<170> FastSEQ for Windows Version 3.0

20 <210> 1

<211> 1164

<212> PRT

<213> Streptococcus pyogenes

25 <400> 1

Leu Arg Lys Lys Gln Lys Leu Pro Phe Asp Lys Leu Ala Ile Ala Leu
1 5 10 15

Met Ser Thr Ser Ile Leu Leu Asn Ala Gln Ser Asp Ile Lys Ala Asn
20 25 30

30 Thr Val Thr Glu Asp Thr Pro Ala Thr Glu Gln Ala Val Glu Thr Pro
35 40 45

Gln Pro Thr Thr Val Ser Glu Glu Val Pro Ser Ser Lys Glu Thr Lys
50 55 60

65 Thr Pro Gln Thr Pro Asp Asp Ala Glu Glu Thr Val Ala Asp Asp Ala
70 75 80

Asn Asp Leu Ala Pro Gln Ala Pro Ala Lys Thr Pro Asp Thr Ser Ala
85 90 95

100 Thr Ser Lys Ala Thr Ile Arg Asp Leu Asn Asp Pro Ser Gln Val Lys
105 110

40 Thr Leu Gln Glu Lys Ala Gly Lys Gly Ala Gly Thr Val Val Ala Val
115 120 125

Ile Asp Ala Gly Phe Asp Lys Asn His Glu Ala Trp Arg Leu Thr Asp
130 135 140
Lys Ala Lys Ala Arg Tyr Gln Ser Lys Glu Asp Leu Glu Lys Ala Lys
145 150 155 160
5 Lys Glu His Gly Ile Thr Tyr Gly Glu Trp Val Asn Asp Lys Val Ala
165 170 175
Tyr Tyr His Asp Tyr Ser Lys Asp Gly Lys Thr Ala Val Asp Gln Glu
180 185 190
His Gly Thr His Val Ser Gly Ile Leu Ser Gly Asn Ala Pro Ser Glu
10 195 200 205
Thr Lys Glu Pro Tyr Arg Leu Glu Gly Ala Met Pro Glu Ala Gln Leu
210 215 220
Leu Leu Met Arg Val Glu Ile Val Asn Gly Leu Ala Asp Tyr Ala Arg
225 230 235 240
15 Asn Tyr Ala Gln Ala Ile Arg Asp Ala Val Asn Leu Gly Ala Lys Val
245 250 255
Ile Asn Met Ser Phe Gly Asn Ala Ala Leu Ala Tyr Ala Asn Leu Pro
260 265 270
Asp Glu Thr Lys Lys Pro Phe Val Tyr Ala Lys Ser Lys Gly Val Arg
20 275 280 285
Ile Val Thr Thr Ala Gly Asn Asp Ser Ser Phe Gly Gly Lys Thr Arg
290 295 300
Leu Pro Leu Ala Asp His Pro Asp Tyr Gly Val Val Gly Thr Pro Ala
305 310 315 320
25 Ala Ala Asp Ser Thr Leu Thr Val Ala Ser Tyr Ser Pro Asp Asn Gln
325 330 335
Leu Thr Glu Thr Ala Met Val Lys Thr Asp Asp Gln Gln Asp Lys Glu
340 345 350
Met Pro Val Leu Ser Thr Asn Arg Phe Glu Pro Asn Lys Ala Tyr Asp
30 355 360 365
Tyr Ala Tyr Ala Asn Arg Gly Met Lys Glu Asp Asp Phe Lys Asp Val
370 375 380
Lys Gly Lys Ile Ala Leu Ile Glu Arg Ser Asp Ile Asp Phe Thr Asp
385 390 395 400
35 Lys Ile Ala Asn Ala Lys Lys Ala Gly Ala Val Gly Val Leu Ile Tyr
405 410 415
Asp Asn Gln Asp Lys Gly Phe Pro Ile Glu Leu Pro Asn Val Asp Gln
420 425 430
Met Pro Ala Ala Phe Ile Ser Arg Lys Asp Gly Leu Leu Leu Lys Asp
40 435 440 445

Asn Ser Gln Lys Thr Ile Thr Phe Asn Ala Thr Pro Lys Val Leu Pro
 450 455 460
 Thr Ala Ser Gly Thr Lys Leu Ser Arg Phe Ser Ser Trp Gly Leu Thr
 465 470 475 480
 5 Ala Asp Gly Asn Ile Lys Pro Asp Ile Ala Ala Pro Gly Gln Asp Ile
 485 490 495
 Leu Ser Ser Ala Ala Asn Asn Lys Tyr Ala Lys Leu Ser Gly Thr Ser
 500 505 510
 Met Ser Ala Pro Leu Val Ala Val Ile Met Gly Leu Leu Gln Lys Gln
 10 515 520 525
 Tyr Glu Thr Gln Tyr Pro Asp Met Thr Gln Ser Glu Arg Leu Asp Leu
 530 535 540
 Ala Lys Lys Val Leu Met Ser Ser Ala Thr Ala Leu Tyr Asp Glu Asp
 545 550 555 560
 15 Glu Lys Ala Tyr Phe Ser Pro Arg Gln Gln Gly Ala Gly Ala Val Asp
 565 570 575
 Ala Lys Lys Ala Ser Glu Ala Thr Met Tyr Val Thr Asp Lys Asp Asn
 580 585 590
 Thr Ser Ser Lys Val His Leu Asn Asn Val Ser Asp Lys Phe Glu Val
 20 595 600 605
 Thr Val Thr Val His Asn Lys Ser Asp Lys Pro His Glu Leu Tyr Tyr
 610 615 620
 Gln Ala Thr Val Gln Thr Asp Lys Val Asp Gly Lys His Phe Ala Leu
 625 630 635 640
 25 Ala Pro Lys Ala Leu Ile Glu Thr Ser Trp Gln Lys Ile Thr Ile Pro
 645 650 655
 Ala Asn Ser Ser Lys Gln Val Thr Ile Pro Ile Asp Ile Ser Gln Phe
 660 665 670
 Ser Lys Asp Leu Leu Ala Gln Met Lys Asn Gly Tyr Phe Leu Glu Gly
 30 675 680 685
 Phe Val Arg Ile Lys Gln Asp Pro Thr Lys Glu Glu Leu Met Ser Ile
 690 695 700
 Pro Tyr Ile Gly Phe Arg Gly Asp Phe Gly Asn Leu Ser Ala Leu Glu
 705 710 715 720
 35 Lys Pro Leu Tyr Asp Ser Lys Asp Gly Ser Ser Tyr Tyr His Glu Glu
 725 730 735
 Ile Ser Asp Ala Lys Asp Gln Leu Asp Gly Asp Gly Leu Gln Phe Tyr
 740 745 750
 Ala Leu Lys Asn Asp Phe Thr Ala Leu Thr Thr Glu Ser Asn Pro Trp
 40 755 760 765

Thr Ile Ile Asn Val Val Lys Glu Gly Val Glu Asn Ile Glu Asp Ile
 770 775 780
 Glu Ser Ser Glu Ile Thr Glu Thr Ile Phe Ala Gly Thr Phe Ala Lys
 785 790 795 800
 5 Gln Asp Asp Asp Arg His Tyr Tyr Ile His Arg His Ala Asn Gly Lys
 805 810 815
 Pro Tyr Ala Ala Ile Ser Pro Asn Gly Asp Gly Asn Arg Asp Tyr Val
 820 825 830
 Gln Phe His Gly Thr Phe Leu Arg Asn Ala Lys Asn Leu Val Ala Glu
 10 835 840 845
 Val Leu Asp Lys Glu Gly Asn Val Val Trp Thr Ser Glu Val Thr Glu
 850 855 860
 Gln Val Val Lys Asn Tyr Asn Asn Asp Leu Ala Ser Thr Leu Gly Ser
 865 870 875 880
 15 Thr Arg Phe Glu Ile Ser Arg Trp Asp Gly Lys Asp Lys Asp Ala Lys
 885 890 895
 Val Val Ala Asn Gly Thr Tyr Thr Tyr Arg Val Arg Tyr Thr Pro Ile
 900 905 910
 Ser Ser Gly Ala Lys Glu Gln His Thr Asp Phe Asp Val Ile Val Asp
 20 915 920 925
 Asn Thr Thr Pro Glu Val Ala Thr Ser Ala Thr Phe Ser Thr Glu Asp
 930 935 940
 Arg Arg Leu Thr Leu Ala Ser Lys Pro Gln Thr Ser Gln Pro Val Tyr
 945 950 955 960
 25 Arg Glu Arg Ile Ala Tyr Thr Tyr Met Asp Glu Asp Leu Pro Thr Thr
 965 970 975
 Glu Tyr Ile Ser Pro Asn Glu Asp Gly Thr Phe Thr Leu Pro Glu Glu
 980 985 990
 Ala Glu Thr Met Glu Gly Ala Thr Val Pro Leu Lys Met Ser Asp Phe
 30 995 1000 1005
 Thr Tyr Val Val Glu Asp Met Ala Gly Asn Ile Thr Tyr Thr Pro Val
 1010 1015 1020
 Thr Lys Leu Leu Glu Gly His Ser Asn Lys Pro Glu Gln Asp Gly Ser
 1025 1030 1035 1040
 35 Asp Gln Ala Pro Asp Lys Lys Pro Glu Thr Lys Pro Glu Gln Asp Gly
 1045 1050 1055
 Ser Asp Gln Ala Pro Asp Lys Lys Pro Glu Thr Lys Pro Gly Gln Asp
 1060 1065 1070
 Gly Ser Gly Gln Thr Pro Asp Lys Lys Pro Glu Thr Lys Pro Glu Lys
 40 1075 1080 1085

Asp Ser Ser Gly Gln Thr Pro Gly Lys Thr Pro Gln Lys Gly Gln Pro
1090 1095 1100
Ser Arg Thr Leu Glu Lys Arg Ser Ser Lys Arg Ala Leu Ala Thr Lys
1105 1110 1115 1120
5 Ala Ser Thr Arg Asp Gln Leu Pro Thr Thr Asn Asp Lys Asp Thr Asn
1125 1130 1135
Arg Leu His Leu Leu Lys Leu Val Met Thr Thr Phe Phe Leu Gly Leu
1140 1145 1150
Val Ala His Ile Phe Lys Thr Lys Arg Thr Glu Asp
10 1155 1160

<210> 2
<211> 1167
<212> PRT
15 <213> *Streptococcus pyogenes*

<400> 2
Leu Arg Lys Lys Gln Lys Leu Pro Phe Asp Lys Leu Ala Ile Ala Leu
1 5 10 15
20 Met Ser Thr Ser Ile Leu Leu Asn Ala Gln Ser Asp Ile Lys Ala Asn
20 25 30
Thr Val Thr Glu Asp Thr Pro Val Thr Glu Gln Ala Val Glu Thr Pro
35 40 45
Gln Pro Thr Ala Val Ser Glu Glu Val Pro Ser Ser Lys Glu Thr Lys
25 50 55 60
Thr Pro Gln Thr Pro Asp Asp Ala Glu Glu Thr Ile Ala Asp Asp Ala
65 70 75 80
Asn Asp Leu Ala Pro Gln Ala Pro Ala Lys Thr Ala Asp Thr Pro Ala
85 90 95
30 Thr Ser Lys Ala Thr Ile Arg Asp Leu Asn Asp Pro Ser Gln Val Lys
100 105 110
Thr Leu Gln Glu Lys Ala Gly Lys Gly Ala Gly Thr Val Val Ala Val
115 120 125
Ile Asp Ala Gly Phe Asp Lys Asn His Glu Ala Trp Arg Leu Thr Asp
35 130 135 140
Lys Thr Lys Ala Arg Tyr Gln Ser Lys Glu Asp Leu Glu Lys Ala Lys
145 150 155 160
Lys Glu His Gly Ile Thr Tyr Gly Glu Trp Val Asn Asp Lys Val Ala
165 170 175
40 Tyr Tyr His Asp Tyr Ser Lys Asp Gly Lys Thr Ala Val Asp Gln Glu

	180	185	190
	His Gly Thr His Val Ser Gly Ile Leu Ser Gly Asn Ala Pro Ser Glu		
	195	200	205
	Thr Lys Glu Pro Tyr Arg Leu Glu Gly Ala Met Pro Glu Ala Gln Leu		
5	210	215	220
	Leu Leu Met Arg Val Glu Ile Val Asn Gly Leu Ala Asp Tyr Ala Arg		
	225	230	235
	Asn Tyr Ala Gln Ala Ile Arg Asp Ala Val Asn Leu Gly Ala Lys Val		
	245	250	255
10	Ile Asn Met Ser Phe Gly Asn Ala Ala Leu Ala Tyr Ala Asn Leu Pro		
	260	265	270
	Asp Glu Thr Lys Lys Ala Phe Asp Tyr Ala Lys Ser Lys Gly Val Ser		
	275	280	285
	Ile Val Thr Ser Ala Gly Asn Asp Ser Ser Phe Gly Gly Lys Thr Arg		
15	290	295	300
	Leu Pro Leu Ala Asp His Pro Asp Tyr Gly Val Val Gly Thr Pro Ala		
	305	310	315
	Ala Ala Asp Ser Thr Leu Thr Val Ala Ser Tyr Ser Pro Asp Lys Gln		
	325	330	335
20	Leu Thr Glu Thr Ala Met Val Lys Thr Asp Asp Gln Gln Asp Lys Glu		
	340	345	350
	Met Pro Val Leu Ser Thr Asn Arg Phe Glu Pro Asn Lys Ala Tyr Asp		
	355	360	365
	Tyr Ala Tyr Ala Asn Arg Gly Met Lys Glu Asp Asp Phe Lys Asp Val		
25	370	375	380
	Lys Gly Lys Ile Ala Leu Ile Glu Arg Gly Asp Ile Asp Phe Lys Asp		
	385	390	395
	Lys Val Ala Asn Ala Lys Lys Ala Gly Ala Val Gly Val Leu Ile Tyr		
	405	410	415
30	Asp Asn Gln Asp Lys Gly Phe Pro Ile Glu Leu Pro Asn Val Asp Gln		
	420	425	430
	Met Pro Ala Ala Phe Ile Ser Arg Lys Asp Gly Leu Leu Leu Lys Asp		
	435	440	445
	Asn Pro Gln Lys Thr Ile Thr Phe Asn Ala Thr Pro Lys Val Leu Pro		
35	450	455	460
	Thr Ala Ser Gly Thr Lys Leu Ser Arg Phe Ser Ser Trp Gly Leu Thr		
	465	470	475
	Ala Asp Gly Asn Ile Lys Pro Asp Ile Ala Ala Pro Gly Gln Asp Ile		
	485	490	495
40	Leu Ser Ser Val Ala Asn Asn Lys Tyr Ala Lys Leu Ser Gly Thr Ser		

500 505 510
Met Ser Ala Pro Leu Val Ala Gly Ile Met Gly Leu Leu Gln Lys Gln
515 520 525
Tyr Glu Thr Gln Tyr Pro Asp Met Thr Pro Ser Glu Arg Leu Asp Leu
5 530 535 540
Ala Lys Lys Val Leu Met Ser Ser Ala Thr Ala Leu Tyr Asp Glu Asp
545 550 555 560
Glu Lys Ala Tyr Phe Ser Pro Arg Gln Gln Gly Ala Gly Ala Val Asp
565 570 575
10 Ala Lys Lys Ala Ser Ala Ala Thr Met Tyr Val Thr Asp Lys Asp Asn
580 585 590
Thr Ser Ser Lys Val His Leu Asn Asn Val Ser Asp Lys Phe Glu Val
595 600 605
Thr Val Thr Val His Asn Lys Ser Asp Lys Pro Gln Glu Leu Tyr Tyr
15 610 615 620
Gln Ala Thr Val Gln Thr Asp Lys Val Asp Gly Lys His Phe Ala Leu
625 630 635 640
Ala Pro Lys Val Leu Tyr Glu Ala Ser Trp Gln Lys Ile Thr Ile Pro
645 650 655
20 Ala Asn Ser Ser Lys Gln Val Thr Val Pro Ile Asp Ala Ser Arg Phe
660 665 670
Ser Lys Asp Leu Leu Ala Gln Met Lys Asn Gly Tyr Phe Leu Glu Gly
675 680 685
Phe Val Arg Phe Lys Gln Asp Pro Thr Lys Glu Glu Leu Met Ser Ile
25 690 695 700
Pro Tyr Ile Gly Phe Arg Gly Asp Phe Gly Asn Leu Ser Ala Val Glu
705 710 715 720
Lys Pro Ile Tyr Asp Ser Lys Asp Gly Ser Ser Tyr Tyr His Glu Ala
725 730 735
30 Asn Ser Asp Ala Lys Asp Gln Leu Asp Gly Asp Gly Leu Gln Phe Tyr
740 745 750
Ala Leu Lys Asn Asn Phe Thr Ala Leu Thr Thr Glu Ser Asn Pro Trp
755 760 765
Thr Ile Ile Lys Ala Val Lys Glu Gly Val Glu Asn Ile Glu Asp Ile
35 770 775 780
Glu Ser Ser Glu Ile Thr Glu Thr Ile Phe Ala Gly Thr Phe Ala Lys
785 790 795 800
Gln Asp Asp Asp Ser His Tyr Tyr Ile His Arg His Ala Asn Gly Glu
805 810 815
40 Pro Tyr Ala Ala Ile Ser Pro Asn Gly Asp Gly Asn Arg Asp Tyr Val

	820	825	830
	Gln Phe Gln Gly Thr Phe Leu Arg Asn Ala Lys Asn Leu Val Ala Glu		
	835	840	845
	Val Leu Asp Lys Glu Gly Asn Val Val Trp Thr Ser Glu Val Thr Glu		
5	850	855	860
	Gln Val Val Lys Asn Tyr Asn Asn Asp Leu Ala Ser Thr Leu Gly Ser		
	865	870	875
	Thr Arg Phe Glu Lys Thr Arg Trp Asp Gly Lys Asp Lys Asp Gly Lys		
	885	890	895
10	Val Val Ala Asn Gly Thr Tyr Thr Tyr Arg Val Arg Tyr Thr Pro Ile		
	900	905	910
	Ser Ser Gly Ala Lys Glu Gln His Thr Asp Phe Asp Val Ile Val Asp		
	915	920	925
	Asn Thr Thr Pro Glu Val Ala Thr Ser Ala Thr Phe Ser Thr Glu Asp		
15	930	935	940
	Arg Arg Leu Thr Leu Ala Ser Lys Pro Lys Thr Ser Gln Pro Val Tyr		
	945	950	955
	Arg Glu Arg Ile Ala Tyr Thr Tyr Met Asp Glu Asp Leu Pro Thr Thr		
	965	970	975
20	Glu Tyr Ile Ser Pro Asn Glu Asp Gly Thr Phe Thr Leu Pro Glu Glu		
	980	985	990
	Ala Glu Thr Met Glu Gly Ala Thr Val Pro Leu Lys Met Ser Asp Phe		
	995	1000	1005
	Thr Tyr Val Val Glu Asp Met Ala Gly Asn Ile Thr Tyr Thr Pro Val		
25	1010	1015	1020
	Thr Lys Leu Leu Glu Gly His Ser Asn Lys Pro Glu Gln Asp Gly Ser		
	1025	1030	1035
	Gly Gln Thr Pro Asp Lys Lys Pro Glu Ala Lys Pro Glu Gln Asp Gly		
	1045	1050	1055
30	Ser Asp Gln Ala Pro Asp Lys Lys Pro Glu Ala Lys Pro Glu Gln Asp		
	1060	1065	1070
	Gly Ser Gly Gln Thr Pro Asp Lys Lys Pro Glu Thr Lys Pro Glu Lys		
	1075	1080	1085
	Asp Ser Ser Gly Gln Thr Pro Gly Lys Thr Pro Gln Lys Gly Gln Pro		
35	1090	1095	1100
	Ser Arg Thr Leu Glu Lys Arg Ser Ser Lys Arg Ala Leu Ala Thr Lys		
	1105	1110	1115
	Ala Ser Thr Arg Asp Gln Leu Pro Thr Thr Asn Asp Lys Asp Thr Asn		
	1125	1130	1135
40	Arg Leu His Leu Leu Lys Leu Val Met Thr Thr Phe Phe Phe Gly Leu		

1140 1145 1150
Val Ala His Ile Phe Lys Thr Lys Arg Gln Lys Glu Thr Lys Lys
1155 1160 1165

5 <210> 3
<211> 1150
<212> PRT
<213> *Streptococcus agalactiae*

10 <400> 3
Leu Arg Lys Lys Gln Lys Leu Pro Phe Asp Lys Leu Ala Ile Ala Leu
1 5 10 15
Met Ser Thr Ser Ile Leu Leu Asn Ala Gln Ser Asp Ile Lys Ala Asn
20 25 30

15 Thr Val Thr Glu Asp Thr Pro Ala Thr Glu Gln Thr Val Glu Thr Pro
35 40 45
Gln Pro Thr Ala Val Ser Glu Glu Ala Pro Ser Ser Lys Glu Thr Lys
50 55 60
Thr Pro Gln Thr Pro Ser Asp Ala Gly Glu Thr Val Ala Asp Asp Ala
20 65 70 75 80
Asn Asp Leu Ala Pro Gln Ala Pro Ala Lys Thr Ala Asp Thr Pro Ala
85 90 95
Thr Ser Lys Ala Thr Ile Arg Asp Leu Asn Asp Pro Ser Gln Val Lys
100 105 110

25 Thr Leu Gln Glu Lys Ala Gly Lys Gly Ala Gly Thr Val Val Ala Val
115 120 125
Ile Asp Ala Gly Phe Asp Lys Asn His Glu Ala Trp Arg Leu Thr Asp
130 135 140
Lys Thr Lys Ala Arg Tyr Gln Ser Lys Glu Asp Leu Glu Lys Ala Lys
30 145 150 155 160
Lys Glu His Gly Ile Thr Tyr Gly Glu Trp Val Asn Asp Lys Val Ala
165 170 175
Tyr Tyr His Asp Tyr Ser Lys Asp Gly Lys Thr Ala Val Asp Gln Glu
180 185 190
35 His Gly Thr His Val Ser Gly Ile Leu Ser Gly Asn Ala Pro Ser Glu
195 200 205
Thr Lys Glu Pro Tyr Arg Leu Glu Gly Ala Met Pro Glu Ala Gln Leu
210 215 220
Leu Leu Met Arg Val Glu Ile Val Asn Gly Leu Ala Asp Tyr Ala Arg
40 225 230 235 240

Asn Tyr Ala Gln Ala Ile Arg Asp Ala Ile Asn Leu Gly Ala Lys Val
 245 250 255
 Ile Asn Met Ser Phe Gly Asn Ala Ala Leu Ala Tyr Ala Asn Leu Pro
 260 265 270
 5 Asp Glu Thr Lys Lys Ala Phe Asp Tyr Ala Lys Ser Lys Gly Val Ser
 275 280 285
 Ile Val Thr Ser Ala Gly Asn Asp Ser Ser Phe Gly Gly Lys Thr Arg
 290 295 300
 Leu Pro Leu Ala Asp His Pro Asp Tyr Gly Val Val Gly Thr Pro Ala
 10 305 310 315 320
 Ala Ala Asp Ser Thr Leu Thr Val Ala Ser Tyr Ser Pro Asp Lys Gln
 325 330 335
 Leu Thr Glu Thr Val Arg Val Lys Thr Ala Asp Gln Gln Asp Lys Glu
 340 345 350
 15 Met Pro Val Leu Ser Thr Asn Arg Phe Glu Pro Asn Lys Ala Tyr Asp
 355 360 365
 Tyr Ala Tyr Ala Asn Arg Gly Thr Lys Glu Asp Asp Phe Lys Asp Val
 370 375 380
 Lys Gly Lys Ile Ala Leu Ile Glu Arg Gly Asp Ile Asp Phe Lys Asp
 20 385 390 395 400
 Lys Ile Ala Lys Ala Lys Lys Ala Gly Ala Val Gly Val Leu Ile Tyr
 405 410 415
 Asp Asn Gln Asp Lys Gly Phe Pro Ile Glu Leu Pro Asn Val Asp Gln
 420 425 430
 25 Met Pro Ala Ala Phe Ile Ser Arg Lys Asp Gly Leu Leu Leu Lys Asp
 435 440 445
 Asn Pro Gln Lys Thr Ile Thr Phe Asn Ala Thr Pro Lys Val Leu Pro
 450 455 460
 Thr Ala Ser Gly Thr Lys Leu Ser Arg Phe Ser Ser Trp Gly Leu Thr
 30 465 470 475 480
 Ala Asp Gly Asn Ile Lys Pro Asp Ile Ala Ala Pro Gly Gln Asp Ile
 485 490 495
 Leu Ser Ser Val Ala Asn Asn Lys Tyr Ala Lys Leu Ser Gly Thr Ser
 500 505 510
 35 Met Ser Ala Pro Leu Val Ala Gly Ile Met Gly Leu Leu Gln Lys Gln
 515 520 525
 Tyr Glu Thr Gln Tyr Pro Asp Met Thr Pro Ser Glu Arg Leu Asp Leu
 530 535 540
 Ala Lys Lys Val Leu Met Ser Ser Ala Thr Ala Leu Tyr Asp Glu Asp
 40 545 550 555 560

Glu Lys Ala Tyr Phe Ser Pro Arg Gln Gln Gly Ala Gly Ala Val Asp
565 570 575
Ala Lys Lys Ala Ser Ala Ala Thr Met Tyr Val Thr Asp Lys Asp Asn
580 585 590
5 Thr Ser Ser Lys Val His Leu Asn Asn Val Ser Asp Lys Phe Glu Val
595 600 605
Thr Val Asn Val His Asn Lys Ser Asp Lys Pro Gln Glu Leu Tyr Tyr
610 615 620
Gln Ala Thr Val Gln Thr Asp Lys Val Asp Gly Lys His Phe Ala Leu
10 625 630 635 640
Ala Pro Lys Val Leu Tyr Glu Ala Ser Trp Gln Lys Ile Thr Ile Pro
645 650 655
Ala Asn Ser Ser Lys Gln Val Thr Val Pro Ile Asp Ala Ser Arg Phe
660 665 670
15 Ser Lys Asp Leu Leu Ala Gln Met Lys Asn Gly Tyr Phe Leu Glu Gly
675 680 685
Phe Val Arg Phe Lys Gln Asp Pro Lys Lys Glu Glu Leu Met Ser Ile
690 695 700
Pro Tyr Ile Gly Phe Arg Gly Asp Phe Gly Asn Leu Ser Ala Leu Glu
20 705 710 715 720
Lys Pro Ile Tyr Asp Ser Lys Asp Gly Ser Ser Tyr Tyr His Glu Ala
725 730 735
Asn Ser Asp Ala Lys Asp Gln Leu Asp Gly Asp Gly Leu Gln Phe Tyr
740 745 750
25 Ala Leu Lys Asn Asn Phe Thr Ala Leu Thr Thr Glu Ser Asn Pro Trp
755 760 765
Thr Ile Ile Lys Ala Val Lys Glu Gly Val Glu Asn Ile Glu Asp Ile
770 775 780
Glu Ser Ser Glu Ile Thr Glu Thr Ile Leu Ala Gly Thr Phe Ala Lys
30 785 790 795 800
Gln Asp Asp Asp Ser His Tyr Tyr Ile His Arg His Ala Asn Gly Lys
805 810 815
Pro Tyr Ala Ala Ile Ser Pro Asn Gly Asp Gly Asn Arg Asp Tyr Val
820 825 830
35 Gln Phe Gln Gly Thr Phe Leu Arg Asn Ala Lys Asn Leu Val Ala Glu
835 840 845
Val Leu Asp Lys Glu Gly Asn Val Val Trp Thr Ser Glu Val Thr Glu
850 855 860
Gln Val Val Lys Asn Tyr Asn Asn Asp Leu Ala Ser Thr Leu Gly Ser
40 865 870 875 880

12

Thr Arg Phe Glu Lys Thr Arg Trp Asp Gly Lys Asp Lys Asp Gly Lys
 885 890 895
 Val Val Ala Asn Gly Thr Tyr Thr Tyr Arg Val Arg Tyr Thr Pro Ile
 900 905 910
 5 Ser Ser Gly Ala Lys Glu Gln His Thr Asp Phe Asp Val Ile Val Asp
 915 920 925
 Asn Thr Thr Pro Glu Val Ala Thr Ser Ala Thr Phe Ser Thr Glu Asp
 930 935 940
 Arg Arg Leu Thr Leu Ala Ser Lys Pro Lys Thr Ser Gln Pro Val Tyr
 10 945 950 955 960
 Arg Glu Arg Ile Ala Tyr Thr Tyr Met Asp Glu Asp Leu Pro Thr Thr
 965 970 975
 Glu Tyr Ile Ser Pro Asn Glu Asp Gly Thr Phe Thr Leu Pro Glu Glu
 980 985 990
 15 Ala Glu Thr Thr Glu Gly Ala Thr Val Pro Leu Lys Met Ser Asp Phe
 995 1000 1005
 Thr Tyr Val Val Glu Asp Met Ala Gly Asn Ile Thr Tyr Thr Pro Val
 1010 1015 1020
 Thr Lys Leu Leu Glu Gly His Ser Asn Lys Pro Glu Gln Asp Gly Ser
 20 1025 1030 1035 1040
 Asp Gln Ala Pro Asp Lys Lys Pro Glu Ala Lys Pro Glu Gln Asp Gly
 1045 1050 1055
 Ser Gly Gln Thr Pro Asp Lys Lys Thr Glu Thr Lys Pro Glu Lys Asp
 1060 1065 1070
 25 Ser Ser Gly Gln Thr Pro Gly Lys Thr Pro Gln Lys Gly Gln Pro Ser
 1075 1080 1085
 Arg Thr Leu Glu Lys Arg Ser Ser Lys Arg Ala Leu Ala Thr Lys Ala
 1090 1095 1100
 Ser Thr Arg Asp Gln Leu Pro Thr Thr Asn Asp Lys Asp Thr Asn Arg
 30 1105 1110 1115 1120
 Leu His Leu Leu Lys Leu Val Met Thr Thr Phe Phe Leu Gly Leu Val
 1125 1130 1135
 Ala His Ile Phe Lys Thr Lys Arg Gln Lys Glu Thr Lys Lys
 1140 1145 1150

35

<210> 4
 <211> 31
 <212> DNA
 <213> Streptococcus pyogenes

40

13

<400> 4
ggggggggaaat tcgttagcggg tatcatggga c 31

5 <210> 5
<211> 31
<212> DNA
<213> *Streptococcus pyogenes*

<400> 5
10 gggggggaaat tcgggtgctg caatatctgg c 31

<210> 6
<211> 17
<212> DNA
15 <213> *Streptococcus pyogenes*

<400> 6
gtaaaaacgac ggccagt 17

20 <210> 7
<211> 19
<212> DNA
<213> *Streptococcus pyogenes*

25 <400> 7
aaggacgaca cattgcgt 19

<210> 8
<211> 31
30 <212> DNA
<213> *Streptococcus pyogenes*

<400> 8
cccccccgat ccacccaaac cccacaaaact c 31

35 <210> 9
<211> 18
<212> DNA
<213> *Streptococcus pyogenes*

40

<400> 9
gagtggccct ccaatagc

18

5 <210> 10
<211> 35
<212> DNA
<213> *Streptococcus pyogenes*

10 <400> 10
10 ccccccggat ccaatactgt gacagaagac actcc

35

15 <210> 11
<211> 25
<212> DNA
<213> *Streptococcus pyogenes*

<400> 11
tttctggaac tagtatgtct gcgcc

25

20 <210> 12
<211> 41
<212> DNA
<213> *Streptococcus pyogenes*

25 <400> 12
ccccccctcg agatgtaaac gatttgtatc cttgtcatta g

41

30 <210> 13
<211> 25
<212> DNA
<213> *Streptococcus pyogenes*

35 <400> 13
cagtgattga tgctggaaaa gataa
<210> 14
<211> 18
<212> DNA
<213> *Streptococcus pyogenes*

15

14
agctactatc agcaccag 18

15
5 <210> 15
<211> 38
<212> DNA
<213> *Streptococcus pyogenes*

15
10 ccccccgaat tcattactgt gacagaagac actcctgc 38

16
15 <210> 16
<211> 39
<212> DNA
<213> *Streptococcus pyogenes*

16
15 <400> 16
cccccccgat ccttattgtt ctggtttatt agagtggcc 39

17
20 <210> 17
<211> 33
<212> DNA
<213> *Streptococcus pyogenes*

17
25 <400> 17
attgctgctg gtttgataa aaatcatgaa gcg 33

18
25 <210> 18
<211> 18
30 <212> DNA
<213> *Streptococcus pyogenes*

18
35 <400> 18
cactgcaaca acagtccc 18

19
35 <210> 19
<211> 18
<212> DNA
<213> *Streptococcus pyogenes*

16

<400> 19
gaggccggca cacacgtg 18

5 <210> 20
<211> 21
<212> DNA
<213> *Streptococcus pyogenes*

10 <400> 20
ttgatcgaca gcgggtttac c 21

15 <210> 21
<211> 22
<212> DNA
<213> *Streptococcus pyogenes*

20 <400> 21
actgctatgt ctgctccatt ag 22

25 <400> 22
tccagaaaagt ttggcatact tggtagc c 31

30 <210> 22
<211> 31
<212> DNA
<213> *Streptococcus pyogenes*

<400> 23
Leu Arg Lys Lys Gln Lys Leu Pro Phe Asp Lys Leu Ala Ile Ala Leu
35 1 5 10 15
Met Ser Thr Ser Ile Leu Leu Asn Ala Gln Ser Asp Ile Lys Ala Asn
20 25 30
Thr Val Thr Glu Asp Thr Pro Ala Thr Glu Gln Ala Val Glu Thr Pro
35 40 45
40 Gln Pro Thr Ala Val Ser Glu Glu Ala Pro Ser Ser Lys Glu Thr Lys

50	55	60
Thr Pro Gln Thr Pro Asp Asp Ala Glu Glu Thr Ile Ala Asp Asp Ala		
65	70	75
Asn Asp Leu Ala Pro Gln Ala Pro Ala Lys Thr Ala Asp Thr Pro Ala		
5	85	90
Thr Ser Lys Ala Thr Ile Arg Asp Leu Asn Asp Pro Ser Gln Val Lys		
100 105 110		
Thr Leu Gln Glu Lys Ala Gly Lys Gly Ala Gly Thr Val Val Ala Val		
115 120 125		
10 Ile Asp Ala Gly Phe Asp Lys Asn His Glu Ala Trp Arg Leu Thr Asp		
130 135 140		
Lys Thr Lys Ala Arg Tyr Gln Ser Lys Glu Asp Leu Glu Lys Ala Lys		
145	150	155
160 Lys Glu His Gly Ile Thr Tyr Gly Glu Trp Val Asn Asp Lys Val Ala		
15	165	170
175 Tyr Tyr His Asp Tyr Ser Lys Asp Gly Lys Thr Ala Val Asp Gln Glu		
180 185 190		
His Gly Thr His Val Ser Gly Ile Leu Ser Gly Asn Ala Pro Ser Glu		
195 200 205		
20 Thr Lys Glu Pro Tyr Arg Leu Glu Gly Ala Met Pro Glu Ala Gln Leu		
210 215 220		
Leu Leu Met Arg Val Glu Ile Val Asn Gly Leu Ala Asp Tyr Ala Arg		
225	230	235
240 Asn Tyr Ala Gln Ala Ile Ile Asp Ala Val Asn Leu Gly Ala Lys Val		
25	245	250
255 Ile Asn Met Ser Phe Gly Asn Ala Ala Leu Ala Tyr Ala Asn Leu Pro		
260 265 270		
Asp Glu Thr Lys Lys Ala Phe Asp Tyr Ala Lys Ser Lys Gly Val Ser		
275 280 285		
30 Ile Val Thr Ser Ala Gly Asn Asp Ser Ser Phe Gly Gly Lys Thr Arg		
290 295 300		
Leu Pro Leu Ala Asp His Pro Asp Tyr Gly Val Val Gly Thr Pro Ala		
305	310	315
320 Ala Ala Asp Ser Thr Leu Thr Val Ala Ser Tyr Ser Pro Asp Lys Gln		
35	325	330
335 Leu Thr Glu Thr Ala Thr Val Lys Thr Ala Asp Gln Gln Asp Lys Glu		
340 345 350		
Met Pro Val Leu Ser Thr Asn Arg Phe Glu Pro Asn Lys Ala Tyr Asp		
355 360 365		
40 Tyr Ala Tyr Ala Asn Arg Gly Met Lys Glu Asp Asp Phe Lys Asp Val		

370	375	380
Lys Gly Lys Ile Ala Leu Ile Glu Arg Gly Asp Ile Asp Phe Lys Asp		
385	390	395
Lys Ile Ala Asn Ala Lys Lys Ala Gly Ala Val Gly Val Leu Ile Tyr		
5	405	410
Asp Asn Gln Asp Lys Gly Phe Pro Ile Glu Leu Pro Asn Val Asp Gln		
	420	425
Met Pro Ala Ala Phe Ile Ser Arg Lys Asp Gly Leu Leu Leu Lys Glu		
	435	440
10 Asn Pro Gln Lys Thr Ile Thr Phe Asn Ala Thr Pro Lys Val Leu Pro		
	450	455
Thr Ala Ser Gly Thr Lys Leu Ser Arg Phe Ser Ser Trp Gly Leu Thr		
465	470	475
Ala Asp Gly Asn Ile Lys Pro Asp Ile Ala Ala Pro Gly Gln Asp Ile		
15	485	490
Leu Ser Ser Val Ala Asn Asn Lys Tyr Ala Lys Leu Ser Gly Thr Ser		
	500	505
Met Ser Ala Pro Leu Val Ala Gly Ile Met Gly Leu Leu Gln Lys Gln		
	515	520
20 Tyr Glu Thr Gln Tyr Pro Asp Met Thr Pro Ser Glu Arg Leu Asp Leu		
	530	535
Ala Lys Lys Val Leu Met Ser Ser Ala Thr Ala Leu Tyr Asp Glu Asp		
545	550	555
Glu Lys Ala Tyr Phe Ser Pro Arg Gln Gln Gly Ala Gly Ala Val Asp		
25	565	570
Ala Lys Lys Ala Ser Ala Ala Thr Met Tyr Val Thr Asp Lys Asp Asn		
	580	585
Thr Ser Ser Lys Val His Leu Asn Asn Val Ser Asp Lys Phe Glu Val		
	595	600
30 Thr Val Thr Val His Asn Lys Ser Asp Lys Pro Gln Glu Leu Tyr Tyr		
	610	615
Gln Ala Thr Val Gln Thr Asp Lys Val Asp Gly Lys Leu Phe Ala Leu		
625	630	635
Ala Pro Lys Ala Leu Tyr Glu Ala Ser Trp Gln Lys Ile Thr Ile Pro		
35	645	650
Ala Asn Ser Ser Lys Gln Val Thr Ile Pro Ile Asp Val Ser Gln Phe		
	660	665
Ser Lys Asp Leu Leu Ala Pro Met Lys Asn Gly Tyr Phe Leu Glu Gly		
	675	680
40 Phe Val Arg Phe Lys Gln Asp Pro Thr Lys Glu Glu Leu Met Ser Ile		

690	695	700
Pro Tyr Ile Gly Phe Arg Gly Asp Phe Gly Asn Leu Ser Ala Leu Glu		
705	710	715
Lys Pro Ile Tyr Asp Ser Lys Asp Gly Ser Ser Tyr Tyr His Glu Ala		
5	725	730
Asn Ser Asp Ala Lys Asp Gln Leu Asp Gly Asp Gly Leu Gln Phe Tyr		
	740	745
Ala Leu Lys Asn Asn Phe Thr Ala Leu Thr Thr Glu Ser Asn Pro Trp		
	755	760
765		
10	Thr Ile Ile Lys Ala Val Lys Glu Gly Val Glu Asn Ile Glu Asp Ile	
	770	775
780		
Glu Ser Ser Glu Ile Thr Glu Thr Ile Phe Ala Gly Thr Phe Ala Lys		
785	790	795
800		
Gln Asp Asp Asp Ser His Tyr Tyr Ile His Arg His Ala Asn Gly Lys		
15	805	810
815		
Pro Tyr Ala Ala Ile Ser Pro Asn Gly Asp Gly Asn Arg Asp Tyr Val		
	820	825
830		
Gln Phe Gln Gly Thr Phe Leu Arg Asn Ala Lys Asn Leu Val Ala Glu		
	835	840
845		
20	Val Leu Asp Lys Glu Gly Asn Val Val Trp Thr Ser Glu Val Thr Glu	
	850	855
860		
Gln Val Val Lys Asn Tyr Asn Asn Asp Leu Ala Ser Thr Leu Gly Ser		
865	870	875
880		
Thr Arg Phe Glu Lys Thr Arg Trp Asp Gly Lys Asp Lys Asp Gly Lys		
25	885	890
895		
Val Val Ala Asn Gly Thr Tyr Thr Arg Val Arg Tyr Thr Pro Ile		
	900	905
910		
Ser Ser Gly Ala Lys Glu Gln His Thr Asp Phe Asp Val Ile Val Asp		
	915	920
925		
30	Asn Thr Thr Pro Glu Val Ala Thr Ser Ala Thr Phe Ser Thr Glu Asp	
	930	935
940		
Arg Arg Leu Thr Leu Ala Ser Lys Pro Lys Thr Ser Gln Pro Val Tyr		
945	950	955
960		
Arg Glu Arg Ile Ala Tyr Thr Tyr Met Asp Glu Asp Leu Pro Thr Thr		
35	965	970
975		
Glu Tyr Ile Ser Pro Asn Glu Asp Gly Thr Phe Thr Leu Pro Glu Glu		
	980	985
990		
Ala Glu Thr Met Glu Gly Ala Thr Val Pro Leu Lys Met Ser Asp Phe		
	995	1000
1005		
40	Thr Tyr Val Val Glu Asp Met Ala Gly Asn Ile Thr Tyr Thr Pro Val	

1010 1015 1020
Thr Lys Leu Leu Glu Gly His Ser Asn Lys Pro Glu Gln Asp Gly Ser
1025 1030 1035 1040
Asp Gln Ala Pro Asp Lys Lys Pro Glu Thr Lys Pro Glu Gln Asp Gly
5 1045 1050 1055
Ser Gly Gln Ala Pro Asp Lys Lys Pro Glu Thr Lys Pro Glu Gln Asp
1060 1065 1070
Gly Ser Gly Gln Thr Pro Asp Lys Lys Pro Glu Thr Lys Pro Glu Gln
1075 1080 1085
10 Asp Gly Ser Gly Gln Thr Pro Asp Lys Lys Pro Glu Thr Lys Pro Glu
1090 1095 1100
Lys Asp Ser Ser Gly Gln Thr Pro Gly Lys Thr Pro Gln Lys Gly Gln
1105 1110 1115 1120
Pro Ser Arg Thr Leu Glu Lys Arg Ser Ser Lys Arg Ala Leu Ala Thr
15 1125 1130 1135
Lys Ala Ser Thr Arg Asp Gln Leu Pro Thr Thr Asn Asp Lys Asp Thr
1140 1145 1150
Asn Arg Leu His Leu Leu Lys Leu Val Met Thr Thr Phe Phe Leu Gly
1155 1160 1165
20 Leu Val Ala His Ile Phe Lys Thr Lys Arg Thr Lys Lys
1170 1175 1180